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Research Article

Integrating social media and environmental DNA records to enhance surveillance and improve early detection of invasive species

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Abstract

The early detection of invasive species in aquatic ecosystems is particularly challenging with most records of new species made years after their initial invasion, by which time they are already widespread. Recently, early detection tools such as citizen science and environmental DNA have emerged, significantly improving early warnings in aquatic ecosystems. However, there is limited understanding of how these new tools complement each other and how consistent they are. In this study, we present a case study combining social media data mining and environmental DNA (eDNA) to detect new records of the invasive European perch (*Perca fluviatilis*) in mainland Portugal. From 2021 to 2024, we analyzed online angling groups to identify potential new areas of invasion. Later, water samples were collected from several reservoirs and tested for the European perch presence using real-time quantitative PCR. This combined approach detected four new locations of European perch. Moreover, eDNA analysis revealed three new potential populations, while data mining appears to offer near real-time tracking of the species' spread. This work showcases the improved efficiency and early detection benefits of this integrated approach for monitoring freshwater invasive fish, with broader applicability to other invasive species.

Key words: Data mining, detection lag, European Perch, freshwaters, non-native species, Perca fluviatilis, qPCR

Introduction

Biological invasions are a global threat to biodiversity and ecosystem integrity, with adverse economic and societal impacts (Lawler et al. 2006; Lodge et al. 2006; Ehrenfeld 2010; Bradshaw et al. 2016). Furthermore, biological invasions and their impacts are expected to continue to rise on par with current trends of global trade, travel and transport (IPBES 2023). The ideal approach to mitigate the impact of invasive species is to prevent their introduction into new areas (Lodge et al. 2006; Finnoff et al. 2007). Following the introduction of invasive species, there is only

a brief window during which eradication or control measures are both effective and cost-efficient (Martinez et al. 2020). These actions are highly dependent on early detection of invasive species, which plays a critical role in enabling fast response measures, and is identified as a top priority in invasive species management programs (e.g., Vander Zanden et al. 2010; IPBES 2023). Early detection constitutes a challenge particularly in aquatic ecosystems, where new introductions remain hidden beneath the surface, often going undetected for extended periods of time and, consequently, enabling their establishment and spread (McDonald and Thompson 2004; Jerde et al. 2011).

Traditional detection methods, relying on the physical capture of specimens, are often labor-intensive, time-consuming and expensive, leading to a lack of broad geographical and temporal coverage (Amano et al. 2016). Consequently, there is a growing demand for innovative surveying approaches that address these weaknesses while also enabling the early detection of invasive species in freshwater ecosystems (Darling and Mahon 2011). A recent new tool is based on the recovery of environmental DNA (eDNA), i.e., the material that organisms release into their surroundings through processes such as shedding skin cells, secreting mucus, or releasing gametes (Taberlet et al. 2012; Pawlowski et al. 2020). These methods are highly sensitive, making them especially suited for detecting early signs of invasive species (Carim et al. 2019; Duarte et al. 2023) or assessing the success of eradication actions (Davison et al. 2019). Additionally, their efficiency and cost-effectiveness greatly enhance the viability of large-scale monitoring programs (Coble et al. 2019). These approaches can target specific taxa using methods like qPCR or use high-throughput sequencing to characterize biological communities (Taberlet et al. 2012).

The use of eDNA in early detection of invasive species may be particularly advantageous when integrated with other techniques such as social media data mining, which can identify areas of potential concern and guide targeted eDNA sampling efforts (Parrondo et al. 2018). In the digital era, a rising number of recreational anglers turn to internet forums and social networks to share their experiences and connect with people with similar interests (Giovos et al. 2018). Individuals often upload text, photographs and videos relating to their fishing activity to social media, contents that are valuable for fisheries sciences (Vitale et al. 2021; Lennox et al. 2022). Given the key role of anglers in the spread of invasive fish species, particularly in the Iberian Peninsula (Ribeiro et al. 2009; Banha and Anastácio 2015; Banha et al. 2024), this growing source of information may represent a cost-effective source of new records that can be used to track the spatial occurrence of new invasive fishes (Gago et al. 2016; Banha et al. 2017). These data have the potential, not only to complement already existing invasive species monitoring programs and methodologies with few added resources and expenses (Daume 2016; Gago et al. 2016; Allain 2019), but also to work as a sentinel tool for a prompt notice of new introductions, and effort redirection.

In Iberia, freshwater fish are among the most threatened taxonomic group (Costa et al. 2021), with invasive species widely recognized as a major threat (Hermoso and Clavero 2011; Zamora-Marín et al. 2023). However, most recent Iberian studies on freshwater fish invasions have primarily focused on three aspects: reporting first occurrences (Ribeiro and Veríssimo 2014; Banha et al. 2015), assessing their impacts on native fauna (Ribeiro et al. 2021; Gkenas et al. 2022), or mapping their distribution long after establishment (Banha et al. 2017; Martelo et al. 2021). In fact, there is still limited information about the range expansion of recently arrived invasive fish (but see Gago et al. 2016), making it difficult to

identify secondary introductions by anglers within specific regions, limiting effective actions to prevent further spread (Caffrey et al. 2014).

Portuguese freshwaters have been highly invaded by different taxa (Anastácio et al. 2019; Zamora-Marín et al. 2023), with one new fish species introduced approximately every two years over the past two decades (Ribeiro et al. 2009; Banha et al. 2017). Of these, one of the most recently introduced predators is the European perch (*Perca fluviatilis* Linnaeus, 1758). This species was introduced in 1898 in the Azores Archipelago by the Forestry Services to promote angling activities (Goubier et al. 1983; Ribeiro et al. 2009). However, it was first detected on the mainland in 2013 (Banha et al. 2015). This species is native to parts of Asia and Europe but naturally absent in southern European Peninsulas (Stepien et al. 2015). Due to its recreational popularity, it has been introduced in many other regions of Europe (Italy, Spain and Cyprus), Africa (Morocco and South Africa), Asia (China) and Oceania (Australia and New Zealand) (Stepien et al. 2015; Ning et al. 2025) with documented negative impacts on these aquatic ecosystems (Morgan et al. 2002; Morgan et al. 2004). This study aimed to assess whether social media records of European perch could help guide an eDNA-based monitoring campaign targeting this invasive fish and monitor its range expansion across mainland Portugal. Using a recently introduced fish in Portugal as a case study, we sought to show the potential of integrating species records from social media data mining, eDNA-based monitoring, and scientific fishing to evaluate the complementarity between these approaches and identify invasion routes and secondary introduction locations.

Methods

Study area

In 2013, the European perch was confirmed on mainland Portugal for the first time, in a small reservoir in Proença-a-Nova (Industrial Park of Proença-a-Nova - PEPA, 39°43'19.9"N, 7°53'58.6"W), located in the central region of the country (Banha et al. 2015). This remained the only known introduction site until 2021, when a new population was recorded in a large reservoir in Sabugal (40°19'57.8"N, 7°05'27.9"W), situated in a different drainage basin (Fig. 1A).

Data mining

We collected information on anglers' catches of European perch from publicly available social media posts on Facebook™, a popular platform among anglers in Portugal with the largest freshwater angling group hosting over 30,000 members, and YouTube™.

On both social media websites, potentially relevant posts were identified by using the search tool with selected key-words. Search keywords included the species' common name in Portuguese ("perca europeia") and variants, such as "perca", "percilha" and "perche". Additionally on Facebook, searches within fishing-groups, such as "Pesca em Água Doce" and "Big Perch Monster" were conducted to identify posts related to the target species, as these groups harbor large and engaged communities on Portuguese and perch angling, respectively. The dataset included posts since May 2021, when the first record of European perch appeared on Facebook™, until December 2024. All collected posts were manually reviewed to confirm species identification, capture location and date, while the raw data was used

to analyze publication trends through time. Then, only posts explicitly related to recreational fishing for European perch, i.e., videos or photographs of catches of perch were selected for further analysis. For each post, we extracted information on the catch's date and location, and compiled data from the different sources into one final dataset. The data collection process adhered to ethical guidelines for social media use in fisheries research, ensuring no personal information was recorded and no original user content was shared publicly (Monkman et al. 2018).

Fish sampling

To confirm the presence of suspected European perch populations reported on social media, field sampling was conducted in suspected locations in February 2023. Gillnets following the European standard EN 14 757 (CEN 2005) were deployed and left overnight. Subsequent to these results, nearby streams were sampled using electrofishing equipment (Hans Grassl EL 6v2 generator, DC, 600 V) to evaluate potential perch dispersal beyond the reservoirs. Electrofishing was conducted along a 120-meter stretch of the stream using a zigzag wading pattern. All captured fish' total length was measured. Native species were released, while invasive species were euthanized in compliance with local regulations using a clove oil overdose as an anesthetic. The presence of European perch was confirmed by the capture of at least one individual.

Environmental DNA samples collection

Site selection for eDNA analysis was informed by a combination of social media data mining and species distribution records (Fig. 1A, B). Sampling was conducted on reservoirs with known populations of European perch as positive controls, such as Sabugal and PEPA. Nearby and hydrologically connected reservoirs were sampled to prospect the existence of undetected populations. The sampling effort was determined based on water body size: one filtration site in small reservoirs (<15 ha), two in medium (15–150 ha) and five in large reservoirs (>150 ha) or rivers. Sites within each reservoir were selected to be as widely dispersed as possible to maximize detection probability.

Between the 24th of June and the 24th of July of 2023, eDNA samples were collected at 52 sites across the hydrographic basins of the Tagus (32 sites), Douro (13 sites), and Ave (7 sites) (Fig. 1C). At each site, we filtered 30 l of water through a 0.45 µm pore-size filter (GoPro^{TM} High Capacity Groundwater Filter, Proactive, Florida, USA) connected by a plastic hose to a diaphragm water pump (Argaly, Sainte-Helene Du Lac, France) with a flowmeter attached to the pump outlet to monitor the filtered volume. Our target filtration volume (30 l) was set to maximize species detection, as recommended by Cantera et al. (2019). The filtration process was stopped early in the case of filter clogging, which we defined as when the flow rate dropped below 1 l per 5 min. Upon completing the filtration, we loaded 50 ml of preservation buffer (Longmire et al. 1997) into the filter capsule and kept samples at 4 °C until laboratory analysis.

Field campaigns adhered to strict contamination control measures: the hose connecting the filter capsule to the inlet of the pump was decontaminated prior to use and discarded afterwards; the syringe used for loading the buffer was single-use; each filter capsule was capped, labeled and sealed individually inside a

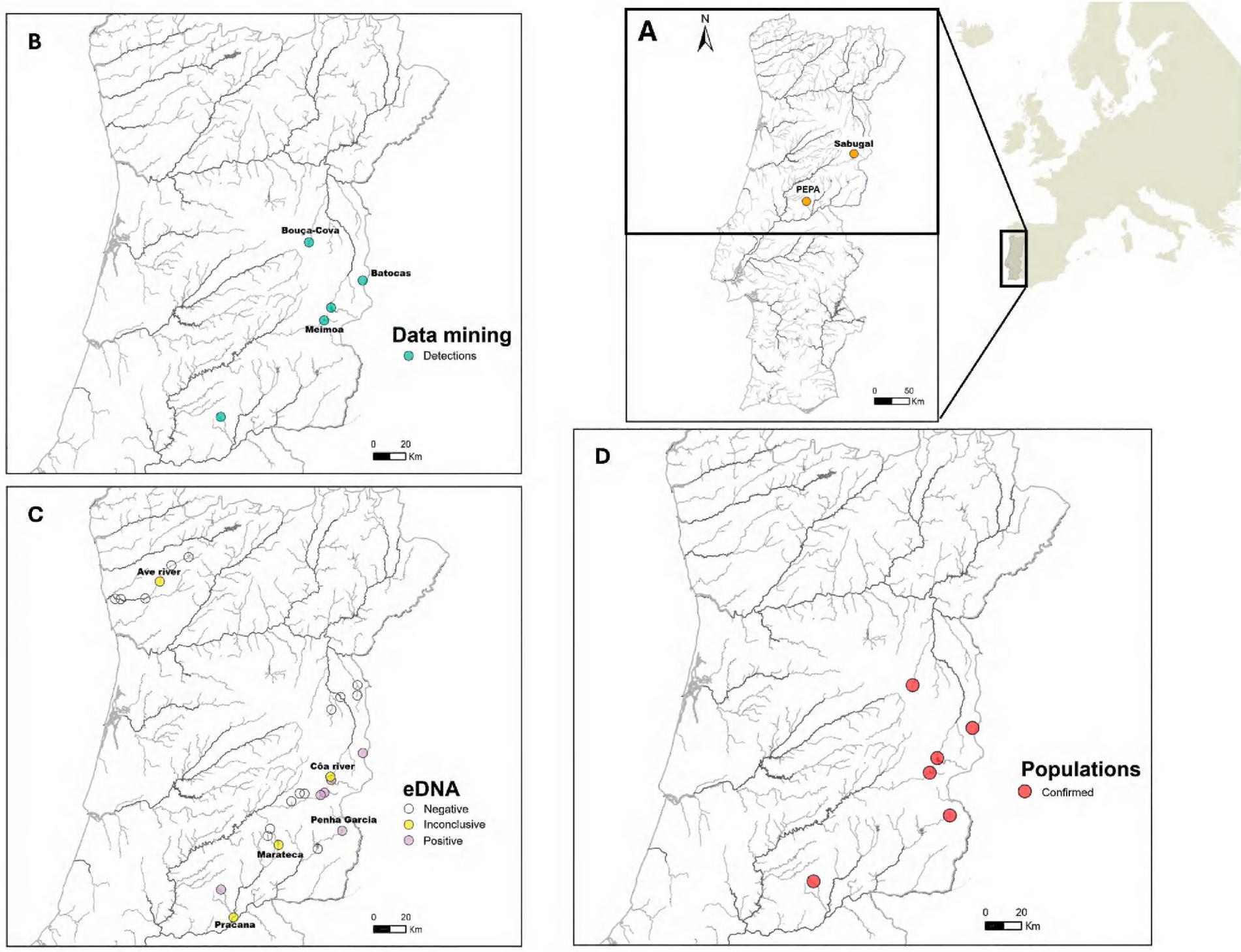

Figure 1. Study area maps of European perch distribution and detections in Portugal: **A.** Known European perch (*Perca fluviatilis*) distribution in Portugal and its relative position in Europe; **B.** Results of social media data mining, where occurrences of European perch were identified through online sources; **C.** Environmental DNA sampling grid and results, where in white are negative results, yellow – inconclusive detections and in purple positive detections; **D.** Confirmed European perch populations through all methods.

decontaminated zipped plastic bag; waders used during sampling were decontaminated between sites; gloves were worn at all times and exchanged between sites or as needed within the same site. Decontamination consisted of soaking the material in a solution of 20% (v/v) commercial bleach for at least 30 min (40% bleach for boots). Field blanks were processed by filtering 6 l of bottled water at the first site each day (one blank per day), following the same protocol as regular samples. A rental car was used, instead of a research institute car, to avoid contamination from previous field trips. Populations identified through social media data mining posteriorly to the eDNA campaign were not sampled for eDNA.

Development of a real-time PCR assay specific for Perca fluviatilis

New primers and probe for the European perch were designed due to the absence of published primers at the time that could provide sufficient specificity for our target species in the study area. The detailed procedure for designing and validating the new primers and probe is provided in Suppl. material 1. Briefly, we compiled sequences for two mitochondrial genes for the Percidae family from National Center for Biotechnology Information (NCBI) nucleotide database (https://www.ncbi.nlm.nih.gov)

and aligned each database using MAFFT (Katoh et al. 2019). PrimerQuest™ was used to identify primer and probe candidate regions in the target species and these regions were subsequently manually refined based on the reference alignments visualized in BioEdit (Hall 1999). Regions were selected with the intent of maximizing mismatches with non-target species, particularly *Sander lucioperca* (the only other percid in the study area), while ensuring no mismatches with the target species. Candidate sets were assessed with OligoAnalyzer™ for thermodynamic properties (Tm, GC content, secondary structures). Specificity was evaluated *in silico* using eDNAssay (Kronenberger et al. 2022) against a comprehensive sequence database of 23 fish species from the study area (also retrieved from NCBI's database). eDNAssay is a freely available web-based tool (https://nationalgenomicscenter.shinyapps.io/eDNAssay) that uses machine learning (random forest models) to predict the likelihood of amplification between a set of primers/probe and a set of DNA sequences. Among all sets tested, the PfluCytb primer-probe set showed the highest amplification probability for *P. fluviatilis* with a very low likelihood of cross-amplification in non-target species. This set of primers (PfluCytb-F: 5'-CCTCCATCCTGGTTCTTATAGTT-3'; and PfluCytb-R: 5'-AGGATAACAACATCTGCGATTAATGT-3') and probe (PfluCytb-P: 5'-ATTGGGAGAGCGGTCGGAATGTAATGCCA-3') targets a 113 base pair region of the Cytochrome b mitochondrial gene. *In vitro* validation was performed on tissue samples from the target species and four sympatric non-target species, including *Sander lucioperca* and other locally abundant taxa. At this stage, no additional percid species were tested beyond those present at our study site, which should be considered when applying this assay in other regions. The qPCR assay was performed using the QuantStudio™ 5 Real-Time PCR System (Thermo Scientific, Massachusetts, USA) under the following protocol: 10 s at 95 °C, followed by 40 cycles of 15 s at 95 °C and 60 s at 60 °C. Each PCR reaction contained a total volume of 10 µl, consisting of 5 µl TaqMan™ Environmental Master Mix 2.0 (Applied Biosystems, California, USA), 0.4 µl each primer (both at 10 µM; Stab Vida, Caparica, Portugal), 0.13 µl of probe (100 µM; Eurofins, Luxembourg), 3.07 µl of sterile ultrapure water, and 1.0 µl of DNA. Reactions were run in duplicate and negative controls included. The PfluCytb set showed clear amplification only in the target species, confirming its specificity.

Assay performance was evaluated using a 5-fold serial dilution of target species' DNA, following the same protocol as above except for the DNA volume (2.0 µl) and water volume (2.07 µl) and all concentrations were run in triplicate. The standard curve demonstrated high linearity (R^2 = 0.9973) and efficiency (101.3%), with Ct variability < 0.3 across replicates.

Laboratory tests of environmental samples

Laboratory processing of the eDNA samples, including DNA extraction and PCR, was conducted in dedicated facilities exclusively used for handling non-invasive samples, meaning material collected without capturing, handling, or directly interacting with the target organism. DNA extractions were performed using the DNeasy Blood and Tissue Kit (Qiagen, Inc., Hilden, Germany), following the manufacturer's guidelines with few modifications detailed in Suppl. material 2. In each extraction batch, 6 randomly chosen samples were processed alongside an extraction blank (from initial 50 ml of Longmire buffer). Extraction success was assessed by agarose gel electrophoresis (0.8%).

All eDNA samples and blanks were tested in triplicate for the presence of European perch using the last protocol described above. Each qPCR run included positive controls (genomic DNA European perch at 78.97 ng/µl) and a negative control (sterile ultrapure water). A replicate was considered positive if an exponential amplification curve was observed (cycle threshold, C_T < 34). In cases where some amplification was observed but the amplification curve did not follow a general exponential pattern), the replicate was considered inconclusive. Sites were deemed positive if at least two replicates displayed C_T values below 34, and negative if none of the replicates showed positive amplification. In cases where only one replicate was positive, or if there were inconclusive results across replicates (e.g., one positive, one inconclusive, and one negative), we considered the presence of European perch in the sample as "Inconclusive".

Given that eDNA detectability can be affected by several environmental factors which can lead to false negatives, we ran two additional qPCR assays, with adjustments in sample input volume. In one essay, we halved the input volume of the sample (1 µl) to reduce the impact of potential inhibitors, and, in the other assay, we used an input sample volume two times higher than in the original assay (4 µl) to account for very low concentrations of eDNA at the sampling sites (Nogueira et al. 2025). These two additional assays were run for all the samples with negative or inconclusive results in the original assays and followed the same protocol as above.

A reservoir/river was classified as positive or inconclusive if at least one site within it yielded a positive or inconclusive result, following a precautionary principle.

Results

A total of 153 social media posts related to European perch were identified between May 2021 and December 2024 (Fig. 2; See Suppl. material 3). Of these, 43 posts were excluded from the species distribution analysis due to the absence of photographic evidence, lack of capture-related content, or references to locations outside mainland Portugal (e.g., the Azores, France, and Spain). These excluded posts typically included fishing-related questions or general information about the species.

The remaining 110 posts (100 from Facebook and 10 from YouTube) were analyzed to determine capture locations based on location tags, post descriptions, comments, and photographic records. In addition to known populations in PEPA and Sabugal, two new locations, Batocas and Meimoa (Figs 1B, 2), were identified in multiple posts between 2021 and 2023. A new reservoir, Bouça Cova, was referenced in posts beginning in July 2024 (Fig. 2). The number of social media posts has increased exponentially over time, with the arrival of the species in new locations triggering a proportional rise in publications. Moreover, the invaded area also increased dramatically with the second location, which is the largest reservoir in surface area and currently this invasive fish has occupied a total of 1000 ha in Portuguese watersheds (Fig. 3).

Fish sampling confirmed the presence of European perch in both Batocas and Meimoa reservoirs. A total of 57 individuals were captured in Batocas and 27 in Meimoa, with sizes ranging from 7.9 cm to 23.7 cm, predominantly comprised by mature individuals. Electrofishing conducted upstream and downstream of the four known population sites (at the time) captured ten European perch upstream of Meimoa reservoir and one individual downstream of the dam. No European perch were detected in streams outside the reservoirs associated with the other three sampled populations (PEPA, Sabugal, and Batocas).

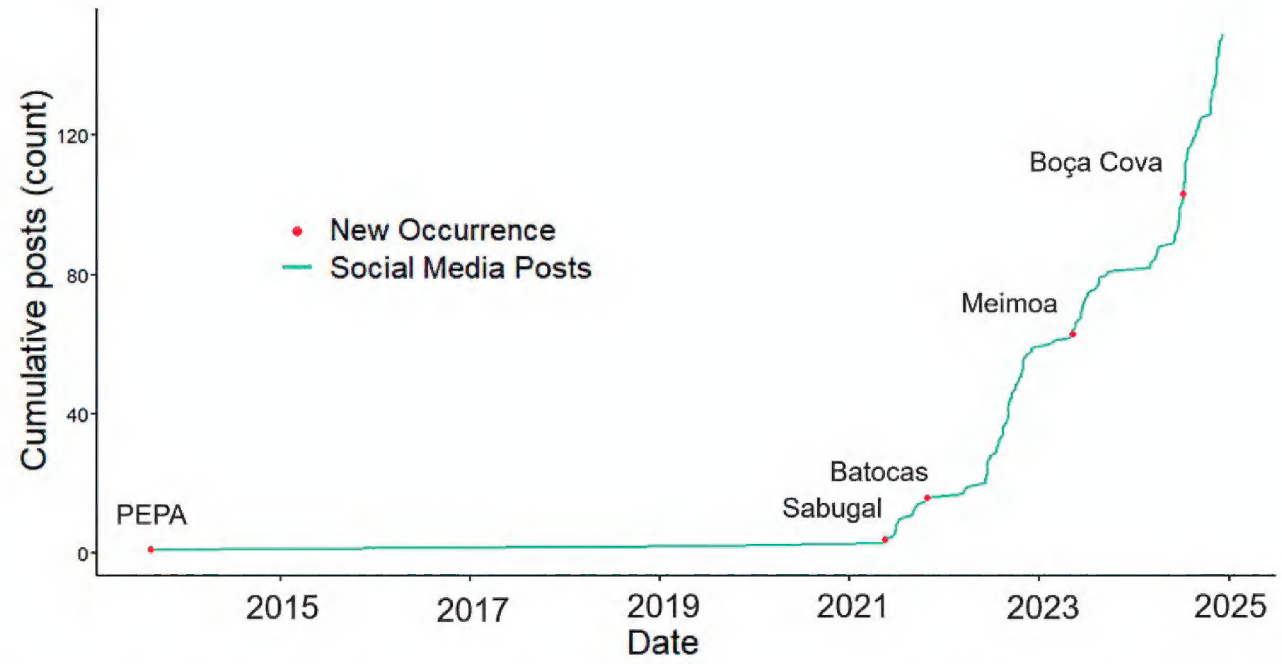

Figure 2. Cumulative social media mentions of European perch: Cumulative number of social media posts detected regarding the European perch through time, with the first occurrence of each population marked in red.

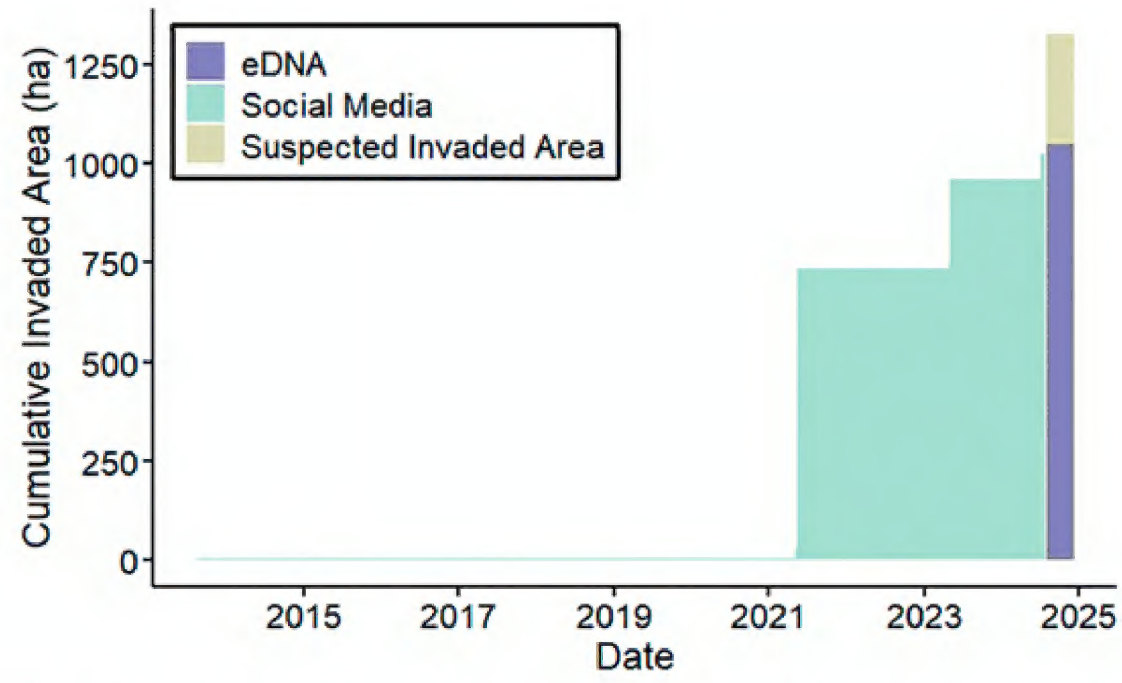

Figure 3. Cumulative invaded area by European perch in Portugal: Cumulative invaded area by European perch through time, with social media assessed detections in green, eDNA positive detections in purple and eDNA inconclusive detections in Yellow.

Under the original qPCR conditions, European perch was detected in 11 of the 52 sampled sites (Fig. 1C, Table 1). In all sites with positive eDNA detections, all three qPCR replicates were positive. All eight sites sampled within the four reservoirs confirmed to host European perch populations tested positive: PEPA (one site), Sabugal (three sites), Meimoa (three sites) and Batocas (one site). The rivers downstream of these reservoirs tested positive in Meimoa and Sabugal, whereas in PEPA and Batocas tested negative. The remaining positive detection represented a new location for this species in Penha Garcia reservoir (Fig. 1C). This occurred at one of the two sites sampled in the reservoir, with the other site at this reservoir yielding an inconclusive result (one positive out of three replicates). Two other reservoirs, Marateca and Pracana, where five sites were sampled within each reservoir, as well as the Ave River, where five sites were sampled along the river, yielded one inconclusive site each for the presence of European perch (Fig. 1C). The additional tests varying sample input resulted in inconclusive detections for one site in Penha Garcia under diluted concentration conditions, and one in Pracana under increased concentration conditions. No European perch DNA was detected in the remaining sites across 11 reservoirs (Fig. 1C). None of the negative controls added showed signal of amplification.

Table 1. Summary of main results by location, including main location coordinates (primarily reservoirs; lotic systems are indicated with *) that are representative of the sampled water body, and the number of filtration sites per location (see Suppl. material 4 for details). European perch detection is reported by method: "X" indicates detection (even if inconclusive), "0" indicates no detection, and "N/A" denotes that the method was not applied at that site. The table also identifies the method by which the species was first detected at each location and evaluates the likelihood of an established European perch population based on the detection evidence.

Main locations (reservoirs/rivers)	Coordinates	Filtration sites	Social media	eDNA	Scientific fishing	1st Suspicion	Presence
Penha-Garcia	40°02'44.3"N, 7°00'54.5"W	2	0	X	N/A	eDNA	Highly likely
Idanha-a-Nova	39°56'41.1"N, 7°12'00.0"W	5	0	0	N/A	–	No evidence
Marateca	39°58'10.2"N, 7°28'57.0"W	5	0	X	0	eDNA	Somewhat likely
Pracana	39°33'54.1"N, 7°48'43.5"W	5	0	X	0	eDNA	Somewhat likely
PEPA	39°43'21.0"N, 7°53'57.6"W	2	X	X	X	Social Media	Confirmed
Pisco	40°01'24.8"N, 7°33'23.6"W	2	0	0	N/A	–	No evidence
P. Redondo	40°03'44.8"N, 7°32'24.8"W	1	0	0	N/A	–	No evidence
Capinha	40°12'53.3"N, 7°22'59.1"W	1	0	0	N/A	–	No evidence
Monte Bispo	40°15'30.9"N, 7°19'23.2"W	1	0	0	N/A	–	No evidence
Escarigo	40°15'25.9"N, 7°17'10.1"W	1	0	0	N/A	–	No evidence
Meimoa	40°15'33.7"N, 7°08'23.7"W	3	X	X	X	Social Media	Confirmed
Meimoa stream*	40°15'33.7"N, 7°08'23.7"W	1	0	X	X	Scientific Fishing	Confirmed
Batocas	40°28'49.9"N, 6°51'18.6"W	2	X	X	X	Social Media	Confirmed
Sabugal	40°19'53.2"N, 7°05'42.5"W	3	X	X	X	Social Media	Confirmed
Côa River*	40°19'53.2"N, 7°05'42.5"W	1	0	X	N/A	eDNA	Highly likely
Vascoveiro	40°42'42.2"N, 7°05'39.0"W	2	0	0	N/A	–	No evidence
Sra do Monforte	40°47'12.7"N, 7°00'43.1"W	1	0	0	N/A	–	No evidence
Vermiosa	40°48'17.7"N, 6°53'20.0"W	2	0	0	N/A	–	No evidence
Sta Maria do Aguiar	40°51'52.7"N, 6°53'09.4"W	2	0	0	N/A	–	No evidence
Ermal	41°35'05.4"N, 8°08'10.1"W	2	0	0	N/A	–	No evidence
Ave River*	41°21'17.2"N, 8°27'21.7"W	5	0	X	N/A	eDNA	Highly likely
Bouça Cova	40°41'59.3"N, 7°14'48.2"W	0	X	N/A	N/A	Social Media	Highly likely

Discussion

In this study, we show that social media data mining of invasive fish can effectively guide targeted eDNA-based monitoring, optimizing the search around known or suspected locations and, consequently, confirm recently established populations. By analyzing nearby locations likely to be colonized, as well as potential fishing hotspots, we identified a total of four unreported populations and three suspected localities of European perch in mainland Portugal (Fig. 1C, D, Table 1). Prior to this work, European perch was known to be present in only two reservoirs (PEPA and Sabugal, Fig. 1A), occupying an area of 714 ha which has currently risen to 1026 ha. This approach significantly reduced the species detection time lag, between its arrival and confirmation in new areas, enabling more timely and effective management responses, such as local containment or local eradication.

The rise of social media has facilitated anglers' sharing of fishing experiences online, creating a valuable and publicly accessible data source (Lennox et al. 2022). By monitoring European perch related publications, we identified previously unknown populations in three reservoirs, Batocas, Meimoa and Bouça Cova (Fig. 1B, Table1). The potential of this approach for monitoring this species was first demonstrated in its first record in mainland Portugal (Banha et al. 2015), which relied on data from online fishing forums. Other studies further demonstrated this with

regards to other species, such as the European catfish (Parrondo et al. 2018; Gkenas et al. 2023) and roach (Ribeiro and Veríssimo 2014). Since its initial detection, only one European perch population had been reported through a fisherman's report to the national environmental agency (ICNF) in 2021. Although not analyzed in this study, social media also offers insights into anglers' perceptions of invasive species and management actions and the respective sentiment analysis could guide communication strategies, improve stakeholder engagement, and help foster public acceptance of management initiatives (Lennox et al. 2022; Sbragaglia et al. 2022). However, social media data mining also has limitations (Ghermandi and Sinclair 2019; Jarić et al. 2020). Posts can lack reliability, and the need for cross-verification remains crucial (Jarić et al. 2020; Lennox et al. 2022). In our analysis, we observed instances of species misidentifications, with common examples including the confusion between European perch and other species such as pikeperch (*Sander lucioperca*) or pumpkinseed perch (*Lepomis gibbosus*), a recurring issue in Portugal (Venturelli et al. 2017). Additionally, many members of the public, particularly within angling communities, still believe that natural biotic communities can be improved and thus do not fully recognize the need to protect biodiversity (Cambray 2003). Distrust of scientific institutions within some fishing communities has also led to the withholding of critical information, such as capture locations, from some anglers in Portugal (Dias D., personal observation). Data availability can also be biased towards popular fishing spots and larger reservoirs, limiting insights into less visited, but ecologically significant areas. This bias is evident in Fig. 2, where publication frequency increased significantly after the discovery of populations in larger reservoirs like Sabugal and Meimoa in comparison to the number of publications regarding smaller reservoirs and more remote sites such as Batocas. Other biases have been reported in the literature such as socio-economic, ethical and demographic (Ghermandi and Sinclair 2019; Jarić et al. 2020), and remain one of the challenges iEcology, "the study of ecological patterns and processes using online data generated for other purposes and stored digitally" (Jarić et al. 2020), still faces.

In this study, eDNA complemented social media data mining. Water was sampled from reservoirs less visited by anglers, addressing the bias previously reported for larger and more popular fishing spots. This resulted in a strong indication of a possible new population in Penha Garcia reservoir (Fig. 1D, Table 1), a site not yet mentioned on social media, underscoring eDNA's potential to uncover species in remote or poorly studied areas (Goldberg et al. 2016). In two other reservoirs and one river, inconclusive eDNA results suggested the possible presence of European perch populations. Although no specimens have been recovered from these two reservoirs, this does not necessarily contradict the eDNA findings. eDNA-based methods are significantly more sensitive than traditional fishing techniques (Goldberg et al. 2016), enabling species detection even in the absence of physical captures. Furthermore, eDNA sampling facilitated the survey of multiple locations within a short timeframe, offering a cost-effective and high-throughput alternative to traditional methods, such as direct observation or captured-based surveys (Loeza-Quintana et al. 2020). By targeting less-accessible reservoirs and early stages of invasion, eDNA provided critical insights that could guide early intervention and management strategies (Harrison et al. 2019). In aquatic environments, eDNA sampled at a river site is the result of local DNA traces and genetic material transported from upstream sources along the river network (Carraro et al. 2020). Therefore, the eDNA detection in downstream reservoirs – Meimoa and Sabugal - may not correlate with local

species presence and should thus warrant regular monitoring to access species dispersal downstream of invaded reservoirs. One potential new population identified through social media (Bouça Cova) was not included in the eDNA sampling because it had not been referenced at the time of the survey campaigns.

Several factors can influence species detection using eDNA (Goldberg et al. 2016; Loeza-Quintana et al. 2020; Burian et al. 2021). To address possible false negatives, we applied a dual strategy in the qPCR assay: testing samples at both diluted and concentrated final volumes. This approach led to inconclusive results for European perch in two additional reservoirs (Fig. 1C). There was no evidence of contamination in the associated blanks of these sites. The lack of reproducibility in these samples may also reflect low concentration of target eDNA due to low species abundance in these systems or heterogeneous dispersal patterns of both the organism and eDNA itself (Pont et al. 2018; Buxton et al. 2021). At one of these sites in the Ave River, where the presence of European perch is not officially recognized, an independent study detected the presence of the European perch using eDNA metabarcoding and metagenomics from a water sample collected in 2020 (Curto et al. 2025). Taken together, these findings constitute stronger evidence that the Ave drainage is worthy of further monitoring and support the possibility that in many of the inconclusive sites the European perch might be indeed present. As the use of eDNA in invasive species management will continue to grow (Abbott et al. 2021), clear guidelines are still needed to define how conservation managers should respond to eDNA detections. Given that capture-based surveys remain the gold standard for confirming species' presence, there is a need to allocate adequate resources to support follow-up efforts when eDNA signals raise concerns.

The European perch is in the early stages of invasion in Portugal. Following the first confirmed record (Banha et al. 2015), there was an eight-year gap before a second population was identified. However, the rate of new population discoveries has accelerated, with four new populations confirmed in the past 18 months and three additional suspected. This rapid spread of an invasive species underscores the urgency for management efforts to control dispersal and mitigate impacts on newly invaded systems (Strayer et al. 2017). Monitoring programs are essential to address the rapid changes in fish communities and to track the distribution of invasive species in freshwater systems (Epanchin-Niell 2017). This study also reports the first confirmed occurrence of European perch in a lotic system in Portugal (Meimoa stream), revealing its ability to bypass dams and colonize downstream habitats. These habitats are particularly vulnerable (Hermoso and Clavero 2011), as they often harbor Iberian endemics lacking natural defenses against novel predators like the European perch (Leunda 2010).

In conclusion, this study demonstrates the strong potential of integrating social media data mining with environmental DNA (eDNA) methods for proactive invasive species management. By expanding the monitoring framework to include both the confirmation of suspected populations and the discovery of previously undocumented ones, we significantly enhanced the detection of European perch. The combined use of social media and eDNA has the potential to be a cost-effective and timely approach to detecting invasive species in newly affected areas, even uncovering locations not initially perceived as spatially connected to known populations, thereby bridging the gap between species introduction and effective management (Fig. 1D, Table 1). This approach not only improves early detection of invasive species but also enables more responsive, targeted, and resource-efficient conservation actions, ensuring that management efforts are both informed and timely.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

DNA extraction of environmental samples collection

Authors: Sofia Batista, Sofia Nogueira

Data type: docx

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Link: https://doi.org/10.3897/neobiota.102.151710.suppl1

Supplementary material 2

Development of a real-time PCR assay specific for Perca fluviatilis

Authors: Sofia Batista, Sofia Nogueira

Data type: docx

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Supplementary material 3

Data mined information from social media

Authors: Diogo Dias

Data type: xlsx

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Supplementary material 4

Summary table of results

Authors: Diogo Dias

Data type: docx

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